Corrected Translation of Claims

1. A method of measuring a structural change in a protein when the protein is contacted with a compound, comprising the steps of:

(a) selecting a domain in the protein;

(b) providing information on an orientation of the domain when the protein is not in contact with the compound;

(c) providing information on an orientation of the domain when the protein is in contact with the compound, by

(i) providing known atomic coordinates for the domain,

(ii) providing axial variations of NMR signals, which are generated from the protein in contact with the compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain; and

(d) measuring the structural change in the protein by a difference between the information on an orientation provided in step (b) and the information on an orientation provided in step (c).

2. The method of measurement according to claim 1, wherein the step (b) is a step of:

(b) providing the information on an orientation of the domain when the protein is not in contact with the compound, by

(v) providing known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in no contact with the compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

3. The method of measurement according to claim 1, wherein the step (b) is a step of

(b) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was not in contact with the compound.

4. The method of measurement according to claim 1, wherein in the step (c), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR

spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

5. The method of measurement according to claim 4, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy(k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR

spectroscopy, and using the $\Delta\delta trosy(k)$ together with the following equation (1):

$$\Delta\delta trosy(k) = \sum S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

$i, j = x, y, z.$

6. The method of measurement according to claim 2, wherein in the step (b), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

7. (Original) The method of measurement according to claim 6, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by making no contact of the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta trosy(k)$ for the kth pair of ^{15}N nuclear spins by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta trosy(k)$ together with the following equation (1):

$$\Delta\delta trosy(k) = \sum S_{ij}\{0.5\ D^{0}_{nh}\ \cos\phi^{k}_{i}\ \cos\phi^{k}_{j} + (2/3)\ \delta_{ij}\} \quad (1)$$

$i, j = x, y, z.$

8. The method according to claim 5 or 7, wherein a structural change in the protein when the protein and the compound are contacted is digitized as degree of orientational change by:

(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein before the protein is contacted with the compound, wherein the first three unit vectors are expressed by

$$\overrightarrow{e_{fx}},\ \overrightarrow{e_{fy}},\ \overrightarrow{e_{fz}}$$

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each

other, by using the information on an orientation of the domain in the protein after the protein is contacted with the compound, wherein the second three unit vectors are expressed by

$$\overrightarrow{e_{bx}}, \quad \overrightarrow{e_{by}}, \quad \overrightarrow{e_{bz}}$$

(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c, and

(xii) giving a degree of orientational change by the following equation:

degree of orientational change = $a^2 + b^2 + c^2$.

9. The method according to claim 2, further comprising a step of identifying a position on the protein to which the compound is bound.

10. The method according to claim 9, wherein the step of identifying a position on the protein to which the compound is bound is carried out by comparing the two-dimensional TROSY NMR spectrum obtained in the step (b) with the two-dimensional TROSY NMR spectrum obtained in the step (c) to detect a spectral change, and identifying an amino acid residue in the protein which has induced the spectral change.

11. The method according to claim 1, wherein the liquid crystalline material comprises a mixture selected from the group consisting of:

a mixture of dimyristoylphosphatidylcholine (DMPC) and dihexanoylphosphatidylcholine (DHPC),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and sodium dodecyl sulfate (SDS),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethyl-ammonium bromide (CTAB),

a mixture of 1,2-di-O-dodecyl-sn-glycero-3-phosphocholine(DIODPC) and 3-(cholamidepropyl)-dimethyl-ammonio-2-hydroxy-1-propane sulfate (CHAPS),

a mixture of n-alkyl-poly(ethyleneglycol)/n-alkylalcohol,

filamentous phage,

a mixture of cetylpyridinium chloride(CPCl)-hexanol-NaCl,

a mixture of cetylpyridinium bromide(CPBr)-hexanol-NaCl,

a purple membrane fragment of Halobacterium spp.,

microcrystalline cellulose, and

polyacrylamide gel.

12. The method according to claim 11, wherein the liquid crystalline material is the mixture of 7.5%(w/v) composed of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethyl-ammonium bromide (CTAB)

13. A method of selecting a compound capable of inducing a structural change in a domain within a protein when the protein is contacted with the compound, comprising the steps of:

(a) selecting a domain in the protein;

(b) providing information on an orientation of the domain when the protein is not in contact with the compound;

(c) providing information on an orientation of the domain when the protein is in contact with the compound, by

(i) providing known atomic coordinates for the domain,

(ii) providing axial variations of NMR signals, which are generated from the protein in contact with the compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain; and

(d) determining if the compound is capable of inducing a structural change in the domain when the protein is contacted with the compound, by making a comparison between the information on an orientation provided in step (b) and the information on an orientation provided in step (c).

14. The method according to claim 13, wherein the step (b) is a step of:

(b) providing the information on an orientation of the domain when the protein is not in contact with the compound by

(v) providing known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in no contact with the compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

15. The method according to claim 13, wherein the step (b) is a step of:

(b) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was not in contact with the compound.

16. The method according to claim 13, wherein in the step (c), the axial variations of NMR signals, which are

generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

17. The method according to claim 16, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta trosy\ (k) = \Sigma S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

i,j = x, y, z.

18. The method according to claim 14, wherein in the step (b), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

19. The method according to claim 18, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the

magnetic field, by making no contact of the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta\text{trosy (k)} = \Sigma S_{ij}\{0.5\ D^{0}_{nh}\ \cos\phi^{k}_{i}\ \cos\phi^{k}_{j} + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

20. The method according to claim 17 or 19, wherein the comparison with respect to the information on an orientation in the step (c) is carried out by:

(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein before the protein is contacted with the compound, wherein the first three unit vectors are expressed by

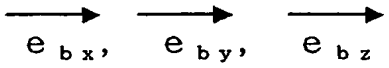
[Formula 22]

$$\overrightarrow{e_{fx}},\ \overrightarrow{e_{fy}},\ \overrightarrow{e_{fz}}$$

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein after the protein is contacted with the

compound, wherein the second three unit vectors are expressed by

[Formula 23]



(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c,

(xii) giving a degree of orientational change by the following equation:

degree of orientational change = $a^2 + b^2 + c^2$

wherein the degree of orientational change is compared.

21. The method according to claim 14, further comprising a step of identifying a position on the protein to which the compound is bound.

22. The method according to claim 21, wherein the step of identifying a position on the protein to which the compound is bound is carried out by comparing the two-dimensional TROSY NMR spectrum obtained in the step (b) with the two-dimensional TROSY NMR spectrum obtained in the step (c) to detect a spectral change, and identifying

an amino acid residue in the protein which has induced the spectral change.

23. The method according to claim 13, wherein the liquid crystalline material comprises a mixture selected from the group consisting of:

a mixture of dimyristoylphosphatidylcholine (DMPC) and dihexanoylphosphatidylcholine (DHPC),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and sodium dodecyl sulfate (SDS),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethylammonium bromide (CTAB),

a mixture of 1,2-di-O-dodecyl-sn-glycero-3-phosphochline (DIODPC) and 3-(cholamidepropyl)-dimethylammonio-2-hydroxy-1-propane sulfate (CHAPS),

a mixture of n-alkyl-poly(ethylene glycol)/n-alkyl alcohol,

filamentous phage,

a mixture of cetylpyridinium chloride (CPCl) - hexanol - NaCl,

a mixture of cetylpyridinium bromide (CPBr) - hexanol - NaCl,

a purple membrane fragment of Halobacterium spp.,

microcrystalline cellulose, and

polyacrylamide gel.

24. The method according to claim 23, wherein the liquid crystalline material is the mixture of 7.5% (w/v) composed of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethylammonium bromide (CTAB).

25. A method of selecting a second compound capable of inducing a structural change in a protein on contact with the protein, which is similar to a structural change in the protein induced by a first compound on contact with the protein, comprising the steps of:

(a) selecting a domain in the protein;

(b) providing information on an orientation of the domain when the protein is in contact with the first compound;

(c) providing information on an orientation of the domain when the protein is in contact with the second compound, by

(i) providing known atomic coordinates for the domain,

(ii) providing axial variations of NMR signals, which are generated from the protein in contact with the second compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain;

(d) making a comparison between the information on an orientation provided in step (b) and the information on an orientation provided in step (c);

and

(e) determining from the results obtained by the comparison in step (d) if the structural change in the protein induced by the second compound on contact with the protein is similar to the structural change in the protein induced by the first compound on contact with the protein.

26. The method according to claim 25, wherein the step (b) is a step of:

(b) providing the information on an orientation of the domain when the protein is in contact with the first compound, by

(v) providing known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in contact with the first compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

27. The method according to claim 25, wherein the step (b) is a step of:

(b) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was in contact with the first compound.

28. The method according to claim 25, wherein the step (c), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

29. The method according to claim 28, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a

static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta\text{trosy (k)} = \Sigma S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

i,j = x, y, z.

30. The method according to claim 26, wherein in the step (b), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

31. The method according to claim 30, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the second compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

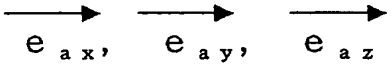
$$\Delta\delta\text{trosy (k)} = \Sigma S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

32. The method according to claim 29 or 31, wherein the comparison with respect to the information on an orientation in the step (d) is carried out by:

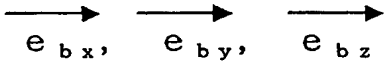
(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the first compound, wherein the first three unit vectors are expressed by

[Formula 24]



(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the second compound, wherein the second three unit vectors are expressed by

[Formula 25]

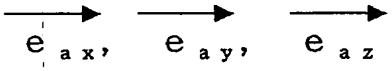


(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c and using the a, b and c as indices for the comparison with respect to the information on an orientation.

33. The method according to claim 29 or 31, wherein the comparison with respect to the information on an orientation in the step (d) is carried out by:

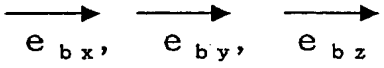
(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the first compound, wherein the first three unit vectors are expressed by

[Formula 26]



(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the second compound, wherein the second three unit vectors are expressed by

[Formula 27]



(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c, and

(xii) giving a degree of orientational similarity to the active conformation by the following equation:

degree of orientational similarity to the active conformation = $a^2 + b^2 + c^2$

wherein the degree of orientational similarity to the active conformation is used as index for the comparison with respect to the information on an orientation.

34. The method according to claim 25, further comprising the step of identifying a position on the protein to which at least one of the first and second compounds is bound.

35. The method according to claim 34, wherein the step of identifying a position on the protein to which at least one of the first and second compounds is bound is carried out by comparing a two-dimensional TROSY NMR spectrum obtained in the absence of the compound with a two-dimensional TROSY NMR spectrum obtained in the presence of the compound to detect a spectral change, and identifying an amino acid residue in the protein which has induced the spectral change.

36. The method according to claim 25, wherein the liquid crystalline material comprises a mixture selected from the group consisting of:

a mixture of dimyristoylphosphatidylcholine (DMPC) and dihexanoylphosphatidylcholine (DHPC),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and sodium dodecyl sulfate (SDS),

a mixture of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethyl-ammonium bromide (CTAB),

a mixture of 1,2-di-O-dodecyl-sn-glycero-3-phosphochline (DIODPC) and 3-(cholamidepropyl)-dimethyl-ammonio-2-hydroxy-1-propane sulfate (CHAPS),

a mixture of n-alkyl-poly(ethylene glycol)/n-alkyl alcohol,

filamentous phage,

a mixture of cetylpyridinium chloride (CPCl) - hexanol - NaCl,

a mixture of cetylpyridinium bromide (CPBr) - hexanol - NaCl,

a purple membrane fragment of Halobacterium spp.,

microcrystalline cellulose, and

polyacrylamide gel.

37. The method according to claim 36, wherein the liquid crystalline material is the mixture of 7.5% (w/v) composed of dimyristoylphosphatidylcholine (DMPC), dihexanoylphosphatidylcholine (DHPC), and cetyltrimethyl-ammonium bromide (CTAB).

38. A program of digitizing a structural change in a selected domain within a protein when the protein is contacted with a compound, comprising carrying out on a computer the means for:

(a) providing information on an orientation of the domain when the protein is not in contact with the compound;

(b) providing information on an orientation of the domain when the protein is in contact with the compound, by

(i) providing data on known atomic coordinates for the domain,

(ii) providing data on axial variations of NMR signals, which are generated from the protein in contact with the compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain; and

(c) calculating the structural change in the protein by a difference between the information on an orientation provided in means (a) and the information on an orientation provided in means (b).

39. The program according to claim 38, wherein the means (a) is means for:

(a) providing information on an orientation of the domain when the protein is not in contact with the compound, by

(v) providing the known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in no contact with the compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

40. The program according to claim 38, wherein the means (a) is means for:

(a) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was not in contact with the compound.

41. The program according to claim 38, wherein in the step (b), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

42. The program according to claim 41, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta\text{trosy (k)} = \Sigma S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

43. The program according to claim 39, wherein in the step (a), the axial variations of NMR signals, which are

generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

44. The program according to claim 43, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by making no contact of the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta trosy\ (k) = \Sigma S_{ij}\{0.5\ D^{0}_{nh}\ \cos\phi^{k}_{i}\ \cos\phi^{k}_{j} + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

45. The program according to claim 42 or 44, wherein a structural change in the protein when the protein and the compound are contacted is digitized as degree of molecular orientational change by:

(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein before the protein is contacted with the compound, wherein the first three unit vectors are expressed by

[Formula 28]

$$\overrightarrow{e_{fx}},\ \overrightarrow{e_{fy}},\ \overrightarrow{e_{fz}}$$

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein after the protein is contacted with the compound, wherein the second three unit vectors are expressed by

[Formula 29]

$$\overrightarrow{e_{bx}},\ \overrightarrow{e_{by}},\ \overrightarrow{e_{bz}}$$

(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c,

(xii) giving a degree of molecular orientational change by the following equation:

degree of molecular orientational change = $a^2 + b^2 + c^2$.

46. The program according to claim 39, further comprising means for identifying a position on the protein to which the compound is bound.

47. The program according to claim 46, wherein the means of identifying a position on the protein to which the compound is bound is carried out by comparing the two-dimensional TROSY NMR spectrum obtained in the step (a) with the two-dimensional TROSY NMR spectrum obtained in the step (b) to detect a spectral change, and identifying an amino acid residue in the protein, which has induced the spectral change.

48. A program of selecting a compound capable of inducing a structural change in a domain within a protein when the protein is contacted with the compound, comprising the means of:

(a) providing information on an orientation of the domain when the protein is not in contact with the compound;

(b) providing information on an orientation of the domain when the protein is in contact with the compound, by

(i) providing known atomic coordinates for the domain,

(ii) providing axial variations of NMR signals, which are generated from the protein in contact with the compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain; and

(c) determining if the compound is capable of inducing a structural change in the domain when the protein is contacted with the compound, by making a comparison between the information on an orientation provided in step (a) and the information on an orientation provided in step (b).

49. The program according to claim 48, wherein the means (a) is means for:

(a) providing information on an orientation of the domain when the protein is not in contact with the compound, by

(v) providing the known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in no contact with the compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

50. The program according to claim 48, wherein the means (a) is means for:

(a) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was not in contact with the compound.

51. The program according to claim 48, wherein in the step (b), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

52. The program according to claim 51, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta\text{trosy (k)} = \Sigma S_{ij}\{0.5\ D^0_{nh}\ \cos\phi^k_i\ \cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

$$i,j = x, y, z.$$

53. The program according to claim 52, wherein in the step (a), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and

depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

54. The program according to claim 53, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by making no contact of the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta trosy\ (k) = \Sigma S_{ij}\{0.5\ D^{0}_{nh}\ cos\phi^{k}_{i}\ cos\phi^{k}_{j} + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

55. The program according to claim 52 or 54, wherein the comparison with respect to the information on an orientation in the step (c) is carried out by:

(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein before the protein is contacted with the compound, wherein the first three unit vectors are expressed by

[Formula 30]

$$\overrightarrow{e_{fx}},\ \overrightarrow{e_{fy}},\ \overrightarrow{e_{fz}}$$

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein after the protein is contacted with the compound, wherein the second three unit vectors are expressed by

[Formula 31]

$$\overrightarrow{e_{bx}},\ \overrightarrow{e_{by}},\ \overrightarrow{e_{bz}}$$

(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c,

(xii) giving a degree of molecular orientational change by the following equation:

degree of molecular orientational change = $a^2 + b^2 + c^2$

wherein the degree of molecular orientational change is compared.

56. The program according to claim 48, further comprising means for identifying a position on the protein to which the compound is bound.

57. The program according to claim 56, wherein the means of identifying a position on the protein to which the compound is bound is carried out by comparing the two-dimensional TROSY NMR spectrum obtained in the step (a) with the two-dimensional TROSY NMR spectrum obtained in the step (b) to detect a spectral change, and identifying an amino acid residue in the protein, which has induced the spectral change.

58. A program of selecting a second compound capable of inducing a structural change in a domain within a protein on contact with the protein, which is similar to a structural change in the domain within the protein induced by a first compound on contact with the protein, comprising the means of:

(a) providing information on an orientation of the domain when the protein is in contact with the first compound;

(b) providing information on an orientation of the domain when the protein is in contact with the second compound, by

(i) providing known atomic coordinates for the domain,

(ii) providing axial variations of NMR signals, which are generated from the protein in contact with the second compound in the presence of a liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in a magnetic field,

(iii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(iv) diagonalizing the determined matrix to produce the information on an orientation of the domain;

(c) making a comparison between the information on an orientation provided in means (a) and the information on an orientation provided in means (b);

and

(d) determining from the results obtained by the comparison in means (c) if the structural change in the protein induced by the second compound on contact with the protein is similar to the structural change in the protein induced by the first compound on contact with the protein.

59. The program according to claim 58, wherein the means (a) is means of:

(a) providing the information on an orientation of the domain when the protein is in contact with the first compound, by

(v) providing known atomic coordinates for the domain,

(vi) providing axial variations of NMR signals, which are generated from the protein in contact with the first compound in the presence of the liquid crystalline material by two-dimensional TROSY NMR spectroscopy and depend on an orientation angle of the molecules in the magnetic field,

(vii) determining Saupe order matrix elements for the domain from the atomic coordinates for the domain and the axial variations of NMR signals, and

(viii) diagonalizing the determined matrix to produce the information on an orientation of the domain.

60. The program according to claim 58, wherein the means (a) is means of:

(a) providing the information on an orientation of the domain from the atomic coordinates provided previously when the protein was in contact with the first compound.

61. The program according to claim 58, wherein in the step (b), the axial variations of NMR signals, which are

generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

62. The program according to claim 61, wherein the Saupe order matrix elements in (iii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the magnetic field, by contacting the protein with the compound in the presence of the liquid crystalline material, providing $\Delta\delta$trosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the $\Delta\delta$trosy (k) together with the following equation (1):

$$\Delta\delta trosy\ (k) = \Sigma S_{ij}\{0.5\ D^0_{nh}\ cos\phi^k_i\ cos\phi^k_j + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

63. The program according to claim 59, wherein in the step (a), the axial variations of NMR signals, which are generated by two-dimensional TROSY NMR spectroscopy and depend on the orientation angle of the molecules in the magnetic field, are variations along a ^{15}N axis.

64. The program according to claim 63, wherein the Saupe order matrix elements in (vii) are determined by:

with respect to the kth pair of ^{15}N nuclear spins in the domain,

providing ϕ^k_i as a vector angle of an N-H bond having the kth pair of spins in the domain to the ith molecular axis,

providing ϕ^k_j as a vector angle of an N-H bond having the kth pair of spins in the domain to the jth molecular axis,

setting a static dipolar coupling D^0_{nh} at 23.0 kHz for a length of the N-H bond of 1.02 Å, or setting a static dipolar coupling D^0_{nh} at 21.7 kHz for a length of the N-H bond of 1.04 Å,

determining as δ_{ij} a tensor value for chemical shift anisotropy of a ^{15}N nucleus in an arbitrary residue of the protein, and

determining the Saupe order matrix elements S_{ij} defining the molecular orientation with respect to the

magnetic field, by contacting the protein with the second compound in the presence of the liquid crystalline material, providing Δδtrosy (k) for the kth pair of ^{15}N nuclear spins of the protein by two-dimensional TROSY NMR spectroscopy, and using the Δδtrosy (k) together with the following equation (1):

$$\Delta\delta trosy\ (k) = \Sigma S_{ij}\{0.5\ D^{0}_{nh}\ \cos\phi^{k}_{i}\ \cos\phi^{k}_{j} + (2/3)\ \delta_{ij}\} \quad (1)$$

$i,j = x, y, z.$

65. The program according to claim 62 or 64, wherein the comparison with respect to the information on an orientation in the step (c) is carried out by:

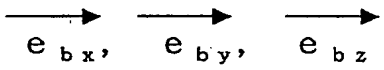
(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the first compound, wherein the first three unit vectors are expressed by

[Formula 32]

$$\overrightarrow{e_{ax}},\ \overrightarrow{e_{ay}},\ \overrightarrow{e_{az}}$$

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the second compound, wherein the second three unit vectors are expressed by

[Formula 33]



(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c and using the a, b and c as indices for the comparison with respect to the information on an orientation.

66. The program according to claim 62 or 64, wherein the comparison with respect to the information on an orientation in the step (c) is carried out by:

(ix) providing directions of orientation tensor axes by a first three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the first compound, wherein the first three unit vectors are expressed by

[Formula 34]

(x) providing directions of orientation tensor axes by a second three unit vectors perpendicular to each other, by using the information on an orientation of the domain in the protein when the protein is contacted with the second compound, wherein the second three unit vectors are expressed by

[Formula 35]

$\overrightarrow{e_{bx}}$, $\overrightarrow{e_{by}}$, $\overrightarrow{e_{bz}}$

(xi) denoting respective angles between the individual first unit vectors and the individual second unit vectors by a, b and c, and

xii) giving a degree of orientational similarity to the active conformation by the following equation:

degree of orientational similarity to the active conformation = $a^2 + b^2 + c^2$

wherein the degree of orientational similarity to the active conformation is used as index for the comparison with respect to the information on an orientation.

67. The program according to claim 58, further comprising the means of identifying a position on the protein to which at least one of the first and second compound is bound.

68. The program according to claim 67, wherein the means of identifying a position on the protein to which at least one of the first and second compound is bound is carried out by comparing a two-dimensional TROSY NMR spectrum obtained in the absence of the compound with a two-dimensional TROSY NMR spectrum obtained in the presence of the compound to detect a spectral change, and identifying an amino acid residue in the protein which has induced the spectral change.

69. An apparatus capable of carrying out the method according to claim 1, 13 or 25.

70. An apparatus provided with the program according to claim 38, 48 or 58.

71. A storage medium containing the program according to claim 38, 48 or 58.